

SEQUENCE LISTING

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<120> Leucine rich repeat containing protein

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<151> 2004-02-12

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<212> DNA

<213> Homo sapiens

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Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe
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Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr
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Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr
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Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu
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Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu
100                      105                      110

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Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu
115                      120                      125

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Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg
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Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu
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Asn Leu Cys Leu Lys Ser Asn Lys Ile Phe Lys Ile Pro Pro Gln Ala
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Phe Lys Asp Leu Lys Lys Leu Gln
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 <213> Homo sapiens

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<211> 584
<212> PRT
<213> Homo sapiens

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Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr
35 40 45
Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg
50 55 60

Arg	Leu	Pro	Arg	Ser	Val	Arg	Ser	Thr	Arg	Asp	Val	Gln	Ala	Ala	Gly	65	70	75	80
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Arg	Leu	Ser	Gly	Ala	Arg	Ala	Glu	Glu	Ala	Leu	Ser	Ala	His	Tyr	Ser	355	360	365	
Glu	Val	Pro	Tyr	Gly	Asp	Pro	Arg	Asp	Thr	Gly	Pro	Ser	Val	Phe	Pro	370	375	380	
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<211> 870
<212> PRT
<213> Homo sapiens

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Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe
35 40 45

Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr
50 55 60

Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr
65 70 75 80

Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu
85 90 95

Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu
100 105 110

Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu
115 120 125

Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg
130 135 140

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Gln	Cys	Asp	Asp	Ser	Val	Ala	Val	Phe	Gln	Asn	Phe	Ile	Ser	Glu	Ser	260	265	270	
Trp	Arg	Lys	Lys	Trp	Asn	Val	Ile	Cys	Asn	Arg	Ser	Ile	Gly	Ser	Glu	275	280	285	
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Pro	Arg	Ser	Val	Arg	Ser	Thr	Arg	Asp	Val	Gln	Ala	Ala	Gly	Lys	Lys	355	360	365	
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	770					775					780					
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785					790					795					800	

Gly Leu Ser Pro Trp Pro Arg Ser Pro Gly Asn Ser Pro Leu Gly Asp
805 810 815

Glu Phe Pro Gly Met Phe Thr Tyr Asp Tyr Asp Thr Ala Leu Gln Ser
820 825 830

Lys Ala Ala Glu Trp His Cys Ser Leu Arg Asp Leu Glu Phe Ser Asn
835 840 845

Val Asp Val Leu Gln Gln Thr Pro Pro Cys Ser Ala Glu Val Pro Ser
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Asp Pro Asp Lys Ala Ala
865 870

<210> 11
<211> 424
<212> DNA
<213> Homo sapiens

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<210> 12
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<213> Homo sapiens

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Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe
35 40 45

Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys
50 55 60

His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro
65 70 75 80

Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala
85 90 95

Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val
100 105 110

Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val
115 120 125

Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly
 130 135 140

<210> 13
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 <212> DNA
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 ttctacgatg acatggaagc tgcggggcac acaccacacc cagagacca tctgcgcaa 1260
 gtatttctct atctaagcct ctacgagaac cagaccctt tctgggtgac acagccacac 1320
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 caggaccaca tccataggaa tgatattctc ggagaatgga cttatgaaac tgtggcccag 1560
 gaagagcctc tcagtgcaca ttcagtgggc gtctctctct tagctggcac gtctcacgct 1620
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 gattatgaca cagctcttca atccaaggca gcagaatggc attgctcact tagagactta 2460
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<210> 14
 <211> 846
 <212> PRT
 <213> Homo sapiens

<400> 14
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 Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe
 35 40 45
 Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys
 50 55 60
 His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro
 65 70 75 80
 Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala
 85 90 95
 Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val
 100 105 110
 Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val
 115 120 125
 Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Leu Trp
 130 135 140
 Lys Leu Lys Ser Leu Gln Ser Leu Asp Leu Ser Phe Asn Gly Ile Leu
 145 150 155 160
 Gln Ile Gly Trp Ser Asp Phe His Asn Cys Leu Gln Leu Glu Asn Leu
 165 170 175
 Cys Leu Lys Ser Asn Lys Ile Phe Lys Ile Pro Pro Gln Ala Phe Lys
 180 185 190
 Asp Leu Lys Lys Leu Gln Val Ile Asp Leu Ser Asn Asn Ala Leu Ile
 195 200 205
 Thr Ile Leu Pro Met Met Ile Ile Ala Leu Glu Phe Pro His Leu Val
 210 215 220
 Val Asp Leu Ala Asp Asn Asn Trp Gln Cys Asp Asp Ser Val Ala Val
 225 230 235 240
 Phe Gln Asn Phe Ile Ser Glu Ser Trp Arg Lys Lys Trp Asn Val Ile
 245 250 255
 Cys Asn Arg Ser Ile Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln
 260 265 270
 Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg
 275 280 285
 Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg
 290 295 300
 His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly
 305 310 315 320
 Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg
 325 330 335

Asp Val Gln Ala Ala Gly Lys Lys Glu Asp Ala Pro Gln Asp Leu Ala
 340 345 350
 Leu Ala Val Cys Leu Ser Val Phe Ile Thr Phe Leu Val Ala Phe Ser
 355 360 365
 Leu Gly Ala Phe Thr Arg Pro Tyr Val Asp Arg Leu Trp Gln Lys Lys
 370 375 380
 Cys Gln Ser Lys Ser Pro Gly Leu Asp Asn Ala Tyr Ser Asn Glu Gly
 385 390 395 400
 Phe Tyr Asp Asp Met Glu Ala Ala Gly His Thr Pro His Pro Glu Thr
 405 410 415
 His Leu Arg Gln Val Phe Pro His Leu Ser Leu Tyr Glu Asn Gln Thr
 420 425 430
 Pro Phe Trp Val Thr Gln Pro His Pro His Ala Thr Val Ile Pro Asp
 435 440 445
 Arg Thr Leu Gly Arg Ser Arg Lys Asp Pro Gly Ser Ser Gln Ser Pro
 450 455 460
 Gly Gln Cys Gly Asp Asn Thr Gly Ala Gly Ser Gly Asn Asp Gly Ala
 465 470 475 480
 Val Tyr Ser Ile Leu Gln Arg His Pro His Ala Gly Asn Arg Glu Leu
 485 490 495
 Met Ser Ala Ala Gln Asp His Ile His Arg Asn Asp Ile Leu Gly Glu
 500 505 510
 Trp Thr Tyr Glu Thr Val Ala Gln Glu Glu Pro Leu Ser Ala His Ser
 515 520 525
 Val Gly Val Ser Ser Val Ala Gly Thr Ser His Ala Val Ser Gly Ser
 530 535 540
 Ser Arg Tyr Asp Ser Asn Glu Leu Asp Pro Ser Leu Ser Gly Glu Ile
 545 550 555 560
 Thr Ala Ser Leu Cys Lys Met Leu Thr His Ala Glu Ala Gln Arg Thr
 565 570 575
 Gly Asp Ser Lys Glu Arg Gly Gly Thr Glu Gln Ser Leu Trp Asp Ser
 580 585 590
 Gln Met Glu Phe Ser Lys Glu Arg Gln Val Ser Ser Ser Ile Asp Leu
 595 600 605
 Leu Ser Ile Gln Gln Pro Arg Leu Ser Gly Ala Arg Ala Glu Glu Ala
 610 615 620
 Leu Ser Ala His Tyr Ser Glu Val Pro Tyr Gly Asp Pro Arg Asp Thr
 625 630 635 640
 Gly Pro Ser Val Phe Pro Pro Arg Trp Asp Ser Gly Leu Asp Val Thr
 645 650 655
 Pro Ala Asn Lys Glu Pro Val Gln Lys Ser Thr Pro Ser Asp Thr Cys

660	665	670	
Cys Glu Leu Glu Ser Asp Cys Asp Ser Asp Glu Gly Ser Leu Phe Thr			
675	680	685	
Leu Ser Ser Ile Ser Ser Glu Ser Ala Arg Ser Lys Thr Glu Glu Ala			
690	695	700	
Val Pro Asp Glu Glu Ser Leu Gln Asp Glu Ser Ser Gly Ala Ser Lys			
705	710	715	720
Asp Asn Val Thr Ala Val Asp Ser Leu Glu Glu Asn Val Thr Phe Gln			
725	730		735
Thr Ile Pro Gly Lys Cys Lys Asn Gln Glu Asp Pro Phe Glu Lys Pro			
740	745		750
Leu Ile Ser Ala Pro Asp Ser Gly Met Tyr Lys Thr His Leu Glu Asn			
755	760		765
Ala Ser Asp Thr Asp Arg Ser Glu Gly Leu Ser Pro Trp Pro Arg Ser			
770	775		780
Pro Gly Asn Ser Pro Leu Gly Asp Glu Phe Pro Gly Met Phe Thr Tyr			
785	790	795	800
Asp Tyr Asp Thr Ala Leu Gln Ser Lys Ala Ala Glu Trp His Cys Ser			
805	810		815
Leu Arg Asp Leu Glu Phe Ser Asn Val Asp Val Leu Gln Gln Thr Pro			
820	825		830
Pro Cys Ser Ala Glu Val Pro Ser Asp Pro Asp Lys Ala Ala			
835	840		845

<210> 15
 <211> 1089
 <212> DNA
 <213> Homo sapiens

<400> 15
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 tatattctga caaattgttc ttttaccgga aagtgtgata tacctgtgga catatcacag 180
 acagcagcca ctgtggatgt aagtttcaat ttcttttagag ttctcttaca gtctcacacg 240
 aaaaaagaag agtggaaaat aaaacatctg gacctcagta acaatctcat atcaaaaata 300
 accttaagcc cttttgcata ttacatgct ttggaagtgt taaacctcag caacaatgcc 360
 atccactccc tctcattgga tctactcagt cctaagtcct catgggtgaa acgccacaga 420
 agcagcttca gaaacaggtt tccattgctg aaggtgctca ttcttcaaag aaataaactc 480
 agtgacactc ccaagggact gtggaaactg aagtcattgc agagtttgga tctgtcattc 540
 aatgggatat tgcaaatagg gtggtctgat tttcacaact gcctgcaact ggagaatctc 600
 tgttttaaaga gcaacaagat attcaaaatt cccccacaag cttcaagga cctcaaaaaa 660
 ttacaggtca tagaccttag caacaatgct ctgattacca tcctaccaat gatgatcata 720
 gctctagaat ttccccatct agtggttgac ttggctgata ataactggca gtgtgatgat 780
 agtgtggcag tctttcaaaa ttttatttct gaatcctgga ggaaaaagtg gaatgtcatt 840
 tgcaacaggt ctataggagg tgaggaggcc aacgggggca ctccccagag caggatttcc 900
 agggaaaccc gccttcctcc cattcatctg catcgcatga aaagcctcat aaggagcaaa 960
 gcagagaggc cccaggagg aaggcacacg ggcatttcta ctctggggaa gaaggcaaag 1020
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 gatgtgcag 1089

<210> 16
 <211> 363
 <212> PRT
 <213> Homo sapiens

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 Phe Thr Gly Ile Met Thr Asn Ala Ser Arg Lys Ser Asn Ile Leu Phe
 20 25 30
 Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe
 35 40 45
 Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr
 50 55 60
 Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr
 65 70 75 80
 Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu
 85 90 95
 Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu
 100 105 110
 Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu
 115 120 125
 Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg
 130 135 140
 Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu
 145 150 155 160
 Ser Asp Thr Pro Lys Gly Leu Trp Lys Leu Lys Ser Leu Gln Ser Leu
 165 170 175
 Asp Leu Ser Phe Asn Gly Ile Leu Gln Ile Gly Trp Ser Asp Phe His
 180 185 190
 Asn Cys Leu Gln Leu Glu Asn Leu Cys Leu Lys Ser Asn Lys Ile Phe
 195 200 205
 Lys Ile Pro Pro Gln Ala Phe Lys Asp Leu Lys Lys Leu Gln Val Ile
 210 215 220
 Asp Leu Ser Asn Asn Ala Leu Ile Thr Ile Leu Pro Met Met Ile Ile
 225 230 235 240
 Ala Leu Glu Phe Pro His Leu Val Val Asp Leu Ala Asp Asn Asn Trp
 245 250 255
 Gln Cys Asp Asp Ser Val Ala Val Phe Gln Asn Phe Ile Ser Glu Ser
 260 265 270
 Trp Arg Lys Lys Trp Asn Val Ile Cys Asn Arg Ser Ile Gly Ser Glu
 275 280 285
 Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg

290 295 300
 Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys
 305 310 315 320
 Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly
 325 330 335
 Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg Arg Leu
 340 345 350
 Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln
 355 360
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 <211> 729
 <212> DNA
 <213> Homo sapiens
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 tatattctga caaattgttc ttttaccgga aagtgtgata tacctgtgga catatcacag 180
 acagcagcca ctgtggatgt aagtttcaat ttcttttagag ttctottaca gtctcacacg 240
 aaaaaagaag agtggaaaat aaaacatctg gacctcagta acaatctcat atcaaaaata 300
 accttaagcc cttttgcata ttacatgct ttggaagtgt taaacctcag caacaatgcc 360
 atccactccc tctcattgga tctactcagt cctaagtcct catgggtgaa acgccacaga 420
 agcagcttca gaaacagggtt tccattgctg aaggtgctca ttcttcaaag aaataaactc 480
 agtgacactc ccaaggggag tgaggaggcc aacgggggca ctccccagag caggatttcc 540
 agggaaaccc gccttctctc cattcatctg catcgcatga aaagcctcat aaggagcaaa 600
 gcagagaggc cccagggagg aaggcacacg ggcatttcta ctctggggaa gaaggcaaag 660
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 <210> 18
 <211> 243
 <212> PRT
 <213> Homo sapiens
 <400> 18
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 Phe Thr Gly Ile Met Thr Asn Ala Ser Arg Lys Ser Asn Ile Leu Phe
 20 25 30
 Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe
 35 40 45
 Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr
 50 55 60
 Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr
 65 70 75 80
 Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu
 85 90 95
 Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu
 100 105 110

Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu
115 120 125

Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg
130 135 140

Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu
145 150 155 160

Ser Asp Thr Pro Lys Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln
165 170 175

Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg
180 185 190

Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg
195 200 205

His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly
210 215 220

Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg
225 230 235 240

Asp Val Gln

<210> 19
<211> 1017
<212> DNA
<213> Homo sapiens

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gtggatgtaa gtttcaattt ctttagagtt ctcttacagt ctcacacgaa aaaagaagag 180
tgaaaaataa aacatctgga cctcagtaac aatctcatat caaaaataac cttaagccct 240
tttgcataatt tacatgcttt ggaagtgtta aacctcagca acaatgccat ccaactccctc 300
tcattggatc tactcagtc taagtcctca tgggtgaaac gccacagaag cagcttcaga 360
aacagggttc cattgctgaa ggtgctcatt cttcaaagaa ataaactcag tgacactccc 420
aagggactgt ggaaactgaa gtcattgcag agtttggatc tgtcattcaa tgggatattg 480
caaatagggt ggtctgattt tcacaactgc ctgcaactgg agaattctctg tttaaagagc 540
aacaagatat tcaaaattcc cccacaagcc ttcaaggacc tcaaaaaatt acaggtcata 600
gaccttagca acaatgctct gattaccatc ctaccaatga tgatcatagc tctagaattt 660
ccccatctag tggttgactt ggctgataat aactggcagt gtgatgatag tgtggcagtc 720
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caggaggagaa ggcacacggg catttctact ctggggaaga aggcaaaggc cggctctggt 960
ctcaggaaga agcagagacg gctgccaagg agtgtagaa gcacccgcga tgtgcag 1017

<210> 20
<211> 339
<212> PRT
<213> Homo sapiens

<400> 20
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1 5 10 15

Tyr Ile Leu Thr Asn Cys Ser Phe Thr Gly Lys Cys Asp Ile Pro Val

<210> 21
 <211> 657
 <212> DNA
 <213> Homo sapiens

<400> 21
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 gtggatgtaa gtttcaattt ctttagagtt ctcttacagt ctcacacgaa aaaagaagag 180
 tggaaaataa aacatctgga cctcagtaac aatctcatat caaaaataac cttaagccct 240
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 tcattggatc tactcagtcc taagtcctca tgggtgaaac gccacagaag cagcttcaga 360
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 aaggggagtg aggaggccaa cggggggaact ccccagagca ggatttccag ggaaacccgc 480
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<210> 22
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 22
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 Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe
 35 40 45
 Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys
 50 55 60
 His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro
 65 70 75 80
 Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala
 85 90 95
 Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val
 100 105 110
 Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val
 115 120 125
 Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Ser Glu
 130 135 140
 Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg
 145 150 155 160
 Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys
 165 170 175
 Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly
 180 185 190

Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg Arg Leu
 195 200 205

Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln
 210 215

<210> 23
 <211> 2628
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> histidine tagged INSP179 nucleotide sequence

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 acagcagcca ctgtggatgt aagtttcaat ttcttttagag ttctcttaca gtctcacacg 240
 aaaaaagaag agtggaaaat aaaacatctg gacctcagta acaatctcat atcaaaaata 300
 accttaagcc cttttgcata tttacatgct ttggaagtgt taaacctcag caacaatgcc 360
 atccactccc tctcattgga tctactcagt cctaagtcct catgggtgaa acgccacaga 420
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 aatgggatat tgcaaatagg gtggtctgat tttcacaact gcctgcaact ggagaatctc 600
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 acaattccag ggaaatgcaa gaatcaagaa gatccctttg aaaaacctct catttctgct 2340
 ccagactctg gcatgtacaa gactcatctg gaaatgcct ctgacactga tagactgag 2400
 ggctgtcac cctggcccag gtcaccagg aatatgcct taggggatga gtttccgggc 2460
 atgttctact atgattatga cacagctctt caatccaagg cagcagaatg gcattgctca 2520
 cttagagact tagaattttc aaatgtggac gttttacagc aaacaccacc atgttctgct 2580
 gaagttccct cagatcctga taaggctgcc caccatcacc atcaccat 2628

<210> 24

<211> 876
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> histidine tagged INSP179 polypeptide sequence

<400> 24

Met	Lys	Asn	Leu	Tyr	Phe	Arg	Val	Ile	Thr	Ile	Val	Ile	Gly	Leu	Tyr	1	5	10	15
Phe	Thr	Gly	Ile	Met	Thr	Asn	Ala	Ser	Arg	Lys	Ser	Asn	Ile	Leu	Phe	20	25	30	
Asn	Ser	Glu	Cys	Gln	Trp	Asn	Glu	Tyr	Ile	Leu	Thr	Asn	Cys	Ser	Phe	35	40	45	
Thr	Gly	Lys	Cys	Asp	Ile	Pro	Val	Asp	Ile	Ser	Gln	Thr	Ala	Ala	Thr	50	55	60	
Val	Asp	Val	Ser	Phe	Asn	Phe	Phe	Arg	Val	Leu	Leu	Gln	Ser	His	Thr	65	70	75	80
Lys	Lys	Glu	Glu	Trp	Lys	Ile	Lys	His	Leu	Asp	Leu	Ser	Asn	Asn	Leu	85	90	95	
Ile	Ser	Lys	Ile	Thr	Leu	Ser	Pro	Phe	Ala	Tyr	Leu	His	Ala	Leu	Glu	100	105	110	
Val	Leu	Asn	Leu	Ser	Asn	Asn	Ala	Ile	His	Ser	Leu	Ser	Leu	Asp	Leu	115	120	125	
Leu	Ser	Pro	Lys	Ser	Ser	Trp	Val	Lys	Arg	His	Arg	Ser	Ser	Phe	Arg	130	135	140	
Asn	Arg	Phe	Pro	Leu	Leu	Lys	Val	Leu	Ile	Leu	Gln	Arg	Asn	Lys	Leu	145	150	155	160
Ser	Asp	Thr	Pro	Lys	Gly	Leu	Trp	Lys	Leu	Lys	Ser	Leu	Gln	Ser	Leu	165	170	175	
Asp	Leu	Ser	Phe	Asn	Gly	Ile	Leu	Gln	Ile	Gly	Trp	Ser	Asp	Phe	His	180	185	190	
Asn	Cys	Leu	Gln	Leu	Glu	Asn	Leu	Cys	Leu	Lys	Ser	Asn	Lys	Ile	Phe	195	200	205	
Lys	Ile	Pro	Pro	Gln	Ala	Phe	Lys	Asp	Leu	Lys	Lys	Leu	Gln	Val	Ile	210	215	220	
Asp	Leu	Ser	Asn	Asn	Ala	Leu	Ile	Thr	Ile	Leu	Pro	Met	Met	Ile	Ile	225	230	235	240
Ala	Leu	Glu	Phe	Pro	His	Leu	Val	Val	Asp	Leu	Ala	Asp	Asn	Asn	Trp	245	250	255	
Gln	Cys	Asp	Asp	Ser	Val	Ala	Val	Phe	Gln	Asn	Phe	Ile	Ser	Glu	Ser	260	265	270	
Trp	Arg	Lys	Lys	Trp	Asn	Val	Ile	Cys	Asn	Arg	Ser	Ile	Gly	Ser	Glu	275	280	285	

Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg
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 Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly
 325 330 335
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 Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln Ala Ala Gly Lys Lys
 355 360 365
 Glu Asp Ala Pro Gln Asp Leu Ala Leu Ala Val Cys Leu Ser Val Phe
 370 375 380
 Ile Thr Phe Leu Val Ala Phe Ser Leu Gly Ala Phe Thr Arg Pro Tyr
 385 390 395 400
 Val Asp Arg Leu Trp Gln Lys Lys Cys Gln Ser Lys Ser Pro Gly Leu
 405 410 415
 Asp Asn Ala Tyr Ser Asn Glu Gly Phe Tyr Asp Asp Met Glu Ala Ala
 420 425 430
 Gly His Thr Pro His Pro Glu Thr His Leu Arg Gln Val Phe Pro His
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 Leu Ser Leu Tyr Glu Asn Gln Thr Pro Phe Trp Val Thr Gln Pro His
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 Pro His Ala Thr Val Ile Pro Asp Arg Thr Leu Gly Arg Ser Arg Lys
 465 470 475 480
 Asp Pro Gly Ser Ser Gln Ser Pro Gly Gln Cys Gly Asp Asn Thr Gly
 485 490 495
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 545 550 555 560
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 Asp Pro Ser Leu Ser Gly Glu Ile Thr Ala Ser Leu Cys Lys Met Leu
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Thr Glu Gln Ser Leu Trp Asp Ser Gln Met Glu Phe Ser Lys Glu Arg
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 Pro Tyr Gly Asp Pro Arg Asp Thr Gly Pro Ser Val Phe Pro Pro Arg
 660 665 670
 Trp Asp Ser Gly Leu Asp Val Thr Pro Ala Asn Lys Glu Pro Val Gln
 675 680 685
 Lys Ser Thr Pro Ser Asp Thr Cys Cys Glu Leu Glu Ser Asp Cys Asp
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 Glu Phe Pro Gly Met Phe Thr Tyr Asp Tyr Asp Thr Ala Leu Gln Ser
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<211> 852

<212> PRT

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<220>

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Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe
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His	Leu	Asp	Leu	Ser	Asn	Asn	Leu	Ile	Ser	Lys	Ile	Thr	Leu	Ser	Pro		
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Phe	Ala	Tyr	Leu	His	Ala	Leu	Glu	Val	Leu	Asn	Leu	Ser	Asn	Asn	Ala		
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Ile	His	Ser	Leu	Ser	Leu	Asp	Leu	Leu	Ser	Pro	Lys	Ser	Ser	Trp	Val		
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Lys	Arg	His	Arg	Ser	Ser	Phe	Arg	Asn	Arg	Phe	Pro	Leu	Leu	Lys	Val		
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Leu	Ile	Leu	Gln	Arg	Asn	Lys	Leu	Ser	Asp	Thr	Pro	Lys	Gly	Leu	Trp		
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Lys	Leu	Lys	Ser	Leu	Gln	Ser	Leu	Asp	Leu	Ser	Phe	Asn	Gly	Ile	Leu		
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Gln	Ile	Gly	Trp	Ser	Asp	Phe	His	Asn	Cys	Leu	Gln	Leu	Glu	Asn	Leu		
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Cys	Leu	Lys	Ser	Asn	Lys	Ile	Phe	Lys	Ile	Pro	Pro	Gln	Ala	Phe	Lys		
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Asp	Leu	Lys	Lys	Leu	Gln	Val	Ile	Asp	Leu	Ser	Asn	Asn	Ala	Leu	Ile		
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Thr	Ile	Leu	Pro	Met	Met	Ile	Ile	Ala	Leu	Glu	Phe	Pro	His	Leu	Val		
	210					215					220						
Val	Asp	Leu	Ala	Asp	Asn	Asn	Trp	Gln	Cys	Asp	Asp	Ser	Val	Ala	Val		
225					230					235					240		
Phe	Gln	Asn	Phe	Ile	Ser	Glu	Ser	Trp	Arg	Lys	Lys	Trp	Asn	Val	Ile		
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Cys	Asn	Arg	Ser	Ile	Gly	Ser	Glu	Glu	Ala	Asn	Gly	Gly	Thr	Pro	Gln		
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Ser	Arg	Ile	Ser	Arg	Glu	Thr	Arg	Leu	Pro	Pro	Ile	His	Leu	His	Arg		
		275					280					285					
Met	Lys	Ser	Leu	Ile	Arg	Ser	Lys	Ala	Glu	Arg	Pro	Gln	Gly	Gly	Arg		
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Leu	Arg	Lys	Lys	Gln	Arg	Arg	Leu	Pro	Arg	Ser	Val	Arg	Ser	Thr	Arg		
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Asp	Val	Gln	Ala	Ala	Gly	Lys	Lys	Glu	Asp	Ala	Pro	Gln	Asp	Leu	Ala		
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Leu	Ala	Val	Cys	Leu	Ser	Val	Phe	Ile	Thr	Phe	Leu	Val	Ala	Phe	Ser		
		355					360					365					
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Cys Gln Ser Lys Ser Pro Gly Leu Asp Asn Ala Tyr Ser Asn Glu Gly				
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Phe Tyr Asp Asp Met Glu Ala Ala Gly His Thr Pro His Pro Glu Thr				
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His Leu Arg Gln Val Phe Pro His Leu Ser Leu Tyr Glu Asn Gln Thr				
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Pro Phe Trp Val Thr Gln Pro His Pro His Ala Thr Val Ile Pro Asp				
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				445
Arg Thr Leu Gly Arg Ser Arg Lys Asp Pro Gly Ser Ser Gln Ser Pro				
		450		455
				460
Gly Gln Cys Gly Asp Asn Thr Gly Ala Gly Ser Gly Asn Asp Gly Ala				
465		470		475
				480
Val Tyr Ser Ile Leu Gln Arg His Pro His Ala Gly Asn Arg Glu Leu				
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Met Ser Ala Ala Gln Asp His Ile His Arg Asn Asp Ile Leu Gly Glu				
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				510
Trp Thr Tyr Glu Thr Val Ala Gln Glu Glu Pro Leu Ser Ala His Ser				
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				525
Val Gly Val Ser Ser Val Ala Gly Thr Ser His Ala Val Ser Gly Ser				
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Ser Arg Tyr Asp Ser Asn Glu Leu Asp Pro Ser Leu Ser Gly Glu Ile				
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Thr Ala Ser Leu Cys Lys Met Leu Thr His Ala Glu Ala Gln Arg Thr				
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Gly Asp Ser Lys Glu Arg Gly Gly Thr Glu Gln Ser Leu Trp Asp Ser				
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				590
Gln Met Glu Phe Ser Lys Glu Arg Gln Val Ser Ser Ser Ile Asp Leu				
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Leu Ser Ile Gln Gln Pro Arg Leu Ser Gly Ala Arg Ala Glu Glu Ala				
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Leu Ser Ala His Tyr Ser Glu Val Pro Tyr Gly Asp Pro Arg Asp Thr				
625		630		635
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Gly Pro Ser Val Phe Pro Pro Arg Trp Asp Ser Gly Leu Asp Val Thr				
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Pro Ala Asn Lys Glu Pro Val Gln Lys Ser Thr Pro Ser Asp Thr Cys				
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Cys Glu Leu Glu Ser Asp Cys Asp Ser Asp Glu Gly Ser Leu Phe Thr				
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Leu Ser Ser Ile Ser Ser Glu Ser Ala Arg Ser Lys Thr Glu Glu Ala				
		690		695
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Val Pro Asp Glu Glu Ser Leu Gln Asp Glu Ser Ser Gly Ala Ser Lys
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Asp Asn Val Thr Ala Val Asp Ser Leu Glu Glu Asn Val Thr Phe Gln
 725 730 735

Thr Ile Pro Gly Lys Cys Lys Asn Gln Glu Asp Pro Phe Glu Lys Pro
 740 745 750

Leu Ile Ser Ala Pro Asp Ser Gly Met Tyr Lys Thr His Leu Glu Asn
 755 760 765

Ala Ser Asp Thr Asp Arg Ser Glu Gly Leu Ser Pro Trp Pro Arg Ser
 770 775 780

Pro Gly Asn Ser Pro Leu Gly Asp Glu Phe Pro Gly Met Phe Thr Tyr
 785 790 795 800

Asp Tyr Asp Thr Ala Leu Gln Ser Lys Ala Ala Glu Trp His Cys Ser
 805 810 815

Leu Arg Asp Leu Glu Phe Ser Asn Val Asp Val Leu Gln Gln Thr Pro
 820 825 830

Pro Cys Ser Ala Glu Val Pro Ser Asp Pro Asp Lys Ala Ala His His
 835 840 845

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 <211> 1107
 <212> DNA
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<220>
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 acagcagcca ctgtggatgt aagtttcaat ttcttttagag ttctcttaca gtctcacacg 240
 aaaaaagaag agtggaataa aaaacatctg gacctcagta acaatctcat atcaaaaata 300
 accttaagcc cttttgcata ttacatgct ttggaagtgt taaacctcag caacaatgcc 360
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 aatgggatat tgcaaataag gtggtctgat tttcacaact gcctgcaact ggagaatctc 600
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<220>
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Asn	Ser	Glu	Cys	Gln	Trp	Asn	Glu	Tyr	Ile	Leu	Thr	Asn	Cys	Ser	Phe	35	40	45	
Thr	Gly	Lys	Cys	Asp	Ile	Pro	Val	Asp	Ile	Ser	Gln	Thr	Ala	Ala	Thr	50	55	60	
Val	Asp	Val	Ser	Phe	Asn	Phe	Phe	Arg	Val	Leu	Leu	Gln	Ser	His	Thr	65	70	75	80
Lys	Lys	Glu	Glu	Trp	Lys	Ile	Lys	His	Leu	Asp	Leu	Ser	Asn	Asn	Leu	85	90	95	
Ile	Ser	Lys	Ile	Thr	Leu	Ser	Pro	Phe	Ala	Tyr	Leu	His	Ala	Leu	Glu	100	105	110	
Val	Leu	Asn	Leu	Ser	Asn	Asn	Ala	Ile	His	Ser	Leu	Ser	Leu	Asp	Leu	115	120	125	
Leu	Ser	Pro	Lys	Ser	Ser	Trp	Val	Lys	Arg	His	Arg	Ser	Ser	Phe	Arg	130	135	140	
Asn	Arg	Phe	Pro	Leu	Leu	Lys	Val	Leu	Ile	Leu	Gln	Arg	Asn	Lys	Leu	145	150	155	160
Ser	Asp	Thr	Pro	Lys	Gly	Leu	Trp	Lys	Leu	Lys	Ser	Leu	Gln	Ser	Leu	165	170	175	
Asp	Leu	Ser	Phe	Asn	Gly	Ile	Leu	Gln	Ile	Gly	Trp	Ser	Asp	Phe	His	180	185	190	
Asn	Cys	Leu	Gln	Leu	Glu	Asn	Leu	Cys	Leu	Lys	Ser	Asn	Lys	Ile	Phe	195	200	205	
Lys	Ile	Pro	Pro	Gln	Ala	Phe	Lys	Asp	Leu	Lys	Lys	Leu	Gln	Val	Ile	210	215	220	
Asp	Leu	Ser	Asn	Asn	Ala	Leu	Ile	Thr	Ile	Leu	Pro	Met	Met	Ile	Ile	225	230	235	240
Ala	Leu	Glu	Phe	Pro	His	Leu	Val	Val	Asp	Leu	Ala	Asp	Asn	Asn	Trp	245	250	255	
Gln	Cys	Asp	Asp	Ser	Val	Ala	Val	Phe	Gln	Asn	Phe	Ile	Ser	Glu	Ser	260	265	270	
Trp	Arg	Lys	Lys	Trp	Asn	Val	Ile	Cys	Asn	Arg	Ser	Ile	Gly	Ser	Glu	275	280	285	

Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg
 290 295 300

Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys
 305 310 315 320

Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly
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<220>
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 accttaagcc cttttgcata tttacatgct ttggaagtgt taaacctcag caacaatgcc 360
 atccactccc tctcattgga tctactcagt cctaagtcct catgggtgaa acgccacaga 420
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 gcagagaggc cccagggagg aaggcacacg ggcatttcta ctctggggaa gaaggcaaag 660
 gccggctctg gtctcaggaa gaagcagaga cggctgccaa ggagtgttag aagcaccgcg 720
 gatgtgcagc accatcacca tcaccat 747

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 <212> PRT
 <213> Artificial Sequence

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Phe Thr Gly Ile Met Thr Asn Ala Ser Arg Lys Ser Asn Ile Leu Phe
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Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe
 35 40 45

Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr

50		55		60
Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr				
65		70		75
Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu				
		85		90
Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu				
		100		105
Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu				
		115		120
Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg				
		130		135
Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu				
		145		150
Ser Asp Thr Pro Lys Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln				
		165		170
Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg				
		180		185
Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg				
		195		200
His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly				
		210		215
Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg				
		225		230
Asp Val Gln His His His His His His				
		245		

<210> 31

<211> 1035

<212> DNA

<213> Artificial Sequence

<220>

<223> histidine tagged INSP179-EC mature nucleotide sequence

<400> 31

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gtggatgtaa	gtttcaattt	ctttagagtt	ctcttacagt	ctcacacgaa	aaaagaagag	180
tggaaaataa	aacatctgga	cctcagtaac	aatctcatat	caaaaataac	cttaagccct	240
tttgcataat	tacatgcttt	ggaagtgtta	aacctcagca	acaatgccat	ccactccctc	300
tcattggatc	tactcagtc	taagtccctca	tgggtgaaac	gccacagaag	cagcttcaga	360
aacaggtttc	cattgctgaa	ggtgctcatt	cttcaaagaa	ataaactcag	tgacactccc	420
aagggactgt	ggaaactgaa	gtcattgcag	agtttggatc	tgtcattcaa	tgggatattg	480
caaatagggt	ggtctgattt	tcacaactgc	ctgcaactgg	agaatctctg	tttaaagagc	540
aacaagatat	tcaaaattcc	cccacaagcc	ttcaaggacc	tcaaaaaatt	acaggtcata	600
gaccttagca	acaatgctct	gattaccatc	ctaccaatga	tgatcatagc	tctagaattt	660
ccccatctag	tggttgactt	ggctgataat	aactggcagt	gtgatgatag	tgtggcagtc	720
tttcaaaatt	ttattttctga	atcctggagg	aaaaagtgga	atgtcatttg	caacagggtct	780
ataggggagt	aggaggccaa	cggggggcact	cccagagca	ggatttccag	ggaaacccgc	840

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cttcctccca ttcatctgca tcgcatgaaa agcctcataa ggagcaaagc agagaggccc 900
cagggaggaa ggcacacggg catttctact ctggggaaga aggcaaaggc cggctctggt 960
ctcaggaaga agcagagacg gctgccaagg agtgtttagaa gcacccgcga tgtgcagcac 1020
catcaccatc accat 1035

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<210> 32
<211> 345
<212> PRT
<213> Artificial Sequence

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<220>
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Tyr Ile Leu Thr Asn Cys Ser Phe Thr Gly Lys Cys Asp Ile Pro Val
20 25 30

Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe
35 40 45

Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys
50 55 60

His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro
65 70 75 80

Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala
85 90 95

Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val
100 105 110

Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val
115 120 125

Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Leu Trp
130 135 140

Lys Leu Lys Ser Leu Gln Ser Leu Asp Leu Ser Phe Asn Gly Ile Leu
145 150 155 160

Gln Ile Gly Trp Ser Asp Phe His Asn Cys Leu Gln Leu Glu Asn Leu
165 170 175

Cys Leu Lys Ser Asn Lys Ile Phe Lys Ile Pro Pro Gln Ala Phe Lys
180 185 190

Asp Leu Lys Lys Leu Gln Val Ile Asp Leu Ser Asn Asn Ala Leu Ile
195 200 205

Thr Ile Leu Pro Met Met Ile Ile Ala Leu Glu Phe Pro His Leu Val
210 215 220

Val Asp Leu Ala Asp Asn Asn Trp Gln Cys Asp Asp Ser Val Ala Val
225 230 235 240

Phe Gln Asn Phe Ile Ser Glu Ser Trp Arg Lys Lys Trp Asn Val Ile
245 250 255

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Cys Asn Arg Ser Ile Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln
260 265 270

Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg
275 280 285

Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg
290 295 300

His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly
305 310 315 320

Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg
325 330 335

Asp Val Gln His His His His His His
340 345

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<211> 675
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<213> Artificial Sequence

<220>
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gtggatgtaa gtttcaattt ctttagagtt ctcttacagt ctcacacgaa aaaagaagag 180
tggaataaa aacatctgga cctcagtaac aatctcatat caaaaataac cttaagccct 240
tttgcattt tactcagtc taagtcctca tgggtgaaac gccacagaag cagcttcaga 300
aacagggttc cattgctgaa ggtgctcatt cttcaaagaa ataaactcag tgacactccc 360
aaggggagtg aggaggccaa cgggggcact cccagagca ggatttccag ggaaaccgcg 420
cttcctccca ttcatctgca tcgcatgaaa agcctcataa ggagcaaagc agagaggccc 480
caggaggaa ggcacacggg catttctact ctggggaaga aggcaaaggc cggctctggt 540
ctcaggaaga agcagagacg gctgccaagg agtgtagaa gcaccgcga tgtgcagcac 600
catcaccatc accat 675

<210> 34
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
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<400> 34
Ser Arg Lys Ser Asn Ile Leu Phe Asn Ser Glu Cys Gln Trp Asn Glu
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Tyr Ile Leu Thr Asn Cys Ser Phe Thr Gly Lys Cys Asp Ile Pro Val
20 25 30
Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe
35 40 45
Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys
50 55 60

His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro
 65 70 75 80
 Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala
 85 90 95
 Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val
 100 105 110
 Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val
 115 120 125
 Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Ser Glu
 130 135 140
 Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg
 145 150 155 160
 Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys
 165 170 175
 Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly
 180 185 190
 Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg Arg Leu
 195 200 205
 Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln His His His His His
 210 215 220

His
225

<210> 35
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> linker sequence

<400> 35
 Glu Phe Gly Ala Gly Leu Val Leu Gly Gly Gln Phe Met
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<210> 36
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer INSP179-CP1

<400> 36
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<210> 37
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 <212> DNA
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<220>
<223> Primer INSP179-CP2

<400> 37
ctgcacatcg cgggtgcttc taac 24

<210> 38
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP179EC-EX1

<400> 38
gcaggcttcg ccacatgaa aaacctctat ttcag 35

<210> 39
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP179EC-EX2

<400> 39
tgatggtgat ggtgctgcac atcgcggtg cttct 35

<210> 40
<211> 29
<212> DNA
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<220>
<223> Primer INSP179-SP1

<400> 40
atgaaaaacc tctatttcag agtcattac 29

<210> 41
<211> 20
<212> DNA
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<220>
<223> Primer INSP179-SP2

<400> 41
caagccttca aggacctcaa 20

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP179-SP3

<400> 42
catgcgatgc agatgaatgg 20

<210> 43
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GCP Forward

<400> 43
ggggacaagt ttgtacaaaa aagcaggctt cgccacc 37

<210> 44
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GCP Reverse

<400> 44
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<210> 45
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<220>
<223> Primer pEAK12F

<400> 45
gccagcttgg cacttgatgt 20

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer pEAK12R

<400> 46
gatggaggtg gacgtgtcag 20

<210> 47
<211> 18
<212> DNA
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<220>
<223> Primer 21M13

<400> 47
tgtaaaacga cggccagt 18

<210> 48
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer M13REV

<400> 48

caggaaacag ctatgacc

18

<210> 49

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer T7

<400> 49

taatacgact cactatagg

19

<210> 50

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer T3

<400> 50

attaaccctc actaaagg

18